1600

```
 3 <110> APPLICANT: COBB, MELANIE
 4        HUTCHISON, MICHELE
 5        ZHU, CHEN
 6        BERMAN, KEVIN
 8 <120> TITLE OF INVENTION: TAO PROTEIN KINASE POLYPEPTIDES AND METHODS OF UE
 9        THEREFOR
11 <130> FILE REFERENCE: UTSD:1276USC1
13 <140> CURRENT APPLICATION NUMBER: 09/686,346B
14 <141> CURRENT FILING DATE: 2000-10-10
16 <150> PRIOR APPLICATION NUMBER: 09/060,410
17 <151> PRIOR FILING DATE: 1998-04-14
19 <160> NUMBER OF SEQ ID NOS: 28
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3312
25 <212> TYPE: DNA
26 <213> ORGANISM: Rattus norvegicus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (121)..(3123)
32 <400> SEQUENCE: 1
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35 tgaaccaagc tttgggatag cagtataaaa ttagaatcag acagctgact gctcagcagg 120
37 atg cca tca act aac aga gca ggc agt cta aag gac cct gaa atc gca     168
38 Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala
39  1               5                   10                  15
41 gag ctc ttc ttc aaa gaa gat ccg gaa aaa ctc ttc aca gat ctc aga     216
42 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg
43              20                  25                  30
45 gaa atc ggc cat ggg agc ttt gga gca gtt tat ttt gca cga gat gtg     264
46 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
47          35                  40                  45
49 cgt act aat gaa gtg gtg gcc atc aag aaa atg tct tat agt gga aag     312
50 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
51      50                  55                  60
53 cag tct act gag aaa tgg cag gat att att aag gaa gtc aag ttt cta     360
54 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
55  65                  70                  75                  80
57 caa aga ata aaa cat ccc aac agt ata gaa tac aaa ggc tgc tat tta     408
58 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
59              85                  90                  95
61 cgt gaa cac aca gca tgg ctt gta atg gaa tat tgt tta gga tct gct     456
62 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
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63                100                     105                     110
65  tcg gat tta cta gaa gtt cat aaa aag cca tta caa gaa gtg gaa ata   504
66  Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
67         115                     120                     125
69  gca gca att aca cat ggt gct ctc cag gga tta gct tat tta cat tct   552
70  Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
71      130                     135                     140
73  cat acc atg atc cat aga gat atc aaa gca gga aat atc ctt ctg aca   600
74  His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr
75 145                     150                     155                160
77  gaa cca ggc caa gtg aaa ctt gct gac ttt gga tct gct tcc atg gcc   648
78  Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala
79                165                     170                     175
81  tcc cct gcc aat tct ttt gtg gga aca cca tat tgg atg gcc cca gaa   696
82  Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
83            180                     185                     190
85  gta att tta gcc atg gat gaa gga caa tat gat ggc aaa gtt gat gta   744
86  Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val
87         195                     200                     205
89  tgg tct ctt gga ata aca tgt att gaa tta gcc gag agg aag cct cct   792
90  Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro
91      210                     215                     220
93  tta ttt aat atg aat gca atg agt gcc tta tat cac ata gcc caa aat   840
94  Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn
95 225                     230                     235                240
97  gaa tcc cct aca cta cag tct aat gaa tgg tct gat tat ttt cga aac   888
98  Glu Ser Pro Thr Leu Gln Ser Asn Glu Trp Ser Asp Tyr Phe Arg Asn
99                245                     250                     255
101 ttt gta gat tct tgc ctc cag aaa atc cct caa gat cgc cct aca tca   936
102 Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg Pro Thr Ser
103            260                     265                     270
105 gag gaa ctt tta aag cac atg ttt gtt ctt cga gag cgc cct gaa aca   984
106 Glu Glu Leu Leu Lys His Met Phe Val Leu Arg Glu Arg Pro Glu Thr
107         275                     280                     285
109 gtg tta ata gat ctt att caa agg aca aag gat gca gta aga gag ctg  1032
110 Val Leu Ile Asp Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu
111      290                     295                     300
113 gac aat cta caa tat cga aag atg aag aaa ctc ctt ttc cag gag gca  1080
114 Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala
115 305                     310                     315                320
117 cat aat gga cca gca gta gaa gca cag gaa gaa gag gag gag caa gat  1128
118 His Asn Gly Pro Ala Val Glu Ala Gln Glu Glu Glu Glu Glu Gln Asp
119                325                     330                     335
121 cat ggt ggt ggc cgg aca gga aca gta aat agt gtt gga agc aat cag  1176
122 His Gly Gly Gly Arg Thr Gly Thr Val Asn Ser Val Gly Ser Asn Gln
123            340                     345                     350
125 tct atc ccc agt atg tct atc agt gcc agt agc caa agc agc agt gtt  1224
126 Ser Ile Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val
127         355                     360                     365
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RAW SEQUENCE LISTING   DATE: 04/08/2004
PATENT APPLICATION: **US/09/686,346B**   TIME: 16:10:19

Input Set : **D:\Utsd1276.app**
Output Set: **N:\CRF4\04082004\I686346B.raw**

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129 aat agt ctt cca gat gca tcg gat gac aag agt gag cta gac atg atg    1272
130 Asn Ser Leu Pro Asp Ala Ser Asp Asp Lys Ser Glu Leu Asp Met Met
131     370             375                 380
133 gag gga gac cat aca gtg atg tct aac agt tct gtc atc cac tta aaa    1320
134 Glu Gly Asp His Thr Val Met Ser Asn Ser Ser Val Ile His Leu Lys
135 385             390                 395                 400
137 cct gag gag gaa aat tac caa gaa gaa gga gat cct aga aca aga gca    1368
138 Pro Glu Glu Glu Asn Tyr Gln Glu Glu Gly Asp Pro Arg Thr Arg Ala
139             405                 410                 415
141 tca gct cca cag tct cca cct caa gtg tct cgt cac aaa tca cat tat    1416
142 Ser Ala Pro Gln Ser Pro Pro Gln Val Ser Arg His Lys Ser His Tyr
143             420             425                 430
145 cgt aat aga gaa cac ttt gca act ata cga aca gca tca ctg gtt aca    1464
146 Arg Asn Arg Glu His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Thr
147         435                 440                 445
149 aga cag atg caa gaa cat gag cag gac tct gaa ctt aga gaa cag atg    1512
150 Arg Gln Met Gln Glu His Glu Gln Asp Ser Glu Leu Arg Glu Gln Met
151     450                 455                 460
153 tct ggt tat aag cgg atg agg cga cag cat cag aag cag ctg atg act    1560
154 Ser Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Met Thr
155 465             470                 475                 480
157 ctg gaa aat aaa ctg aag gca gaa atg gac gaa cat cgg ctc aga tta    1608
158 Leu Glu Asn Lys Leu Lys Ala Glu Met Asp Glu His Arg Leu Arg Leu
159             485                 490                 495
161 gac aaa gat ctt gaa act cag cgc aac aat ttc gct gca gaa atg gag    1656
162 Asp Lys Asp Leu Glu Thr Gln Arg Asn Asn Phe Ala Ala Glu Met Glu
163             500                 505                 510
165 aaa ctt att aag aaa cac caa gct tct atg gaa aaa gag gct aaa gtg    1704
166 Lys Leu Ile Lys Lys His Gln Ala Ser Met Glu Lys Glu Ala Lys Val
167         515                 520                 525
169 atg gcc aac gag gag aaa aaa ttc caa caa cac att cag gct caa cag    1752
170 Met Ala Asn Glu Glu Lys Lys Phe Gln Gln His Ile Gln Ala Gln Gln
171     530                 535                 540
173 aag aaa gaa ctg aat agc ttt ttg gag tct caa aaa aga gaa tat aaa    1800
174 Lys Lys Glu Leu Asn Ser Phe Leu Glu Ser Gln Lys Arg Glu Tyr Lys
175 545             550                 555                 560
177 ctt cga aaa gag cag ctt aag gag gag ctg aat gaa aac cag agc aca    1848
178 Leu Arg Lys Glu Gln Leu Lys Glu Glu Leu Asn Glu Asn Gln Ser Thr
179             565                 570                 575
181 cct aaa aaa gaa aag cag gaa tgg ctt tca aag cag aag gag aat att    1896
182 Pro Lys Lys Glu Lys Gln Glu Trp Leu Ser Lys Gln Lys Glu Asn Ile
183             580                 585                 590
185 caa cat ttt cag gca gaa gaa gaa gct aat ctt ctt cga cgt caa agg    1944
186 Gln His Phe Gln Ala Glu Glu Glu Ala Asn Leu Leu Arg Arg Gln Arg
187         595                 600                 605
189 cag tat cta gag cta gaa tgt cgt cgc ttc aaa aga aga atg tta ctt    1992
190 Gln Tyr Leu Glu Leu Glu Cys Arg Arg Phe Lys Arg Arg Met Leu Leu
191     610                 615                 620
193 ggt cgg cat aac ttg gaa cag gac ctt gtc agg gag gag tta aac aaa    2040
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194 Gly Arg His Asn Leu Glu Gln Asp Leu Val Arg Glu Glu Leu Asn Lys
195 625             630             635             640
197 agg cag act cag aag gac tta gaa cat gca atg tta ctg cga cag cat   2088
198 Arg Gln Thr Gln Lys Asp Leu Glu His Ala Met Leu Leu Arg Gln His
199             645             650             655
201 gaa tcc atg caa gaa ctg gag ttt cgc cac ctc aac act att cag aag   2136
202 Glu Ser Met Gln Glu Leu Glu Phe Arg His Leu Asn Thr Ile Gln Lys
203             660             665             670
205 atg cgc tgt gag ttg atc aga ctg caa cat caa act gag ctt act aac   2184
206 Met Arg Cys Glu Leu Ile Arg Leu Gln His Gln Thr Glu Leu Thr Asn
207         675             680             685
209 cag ctg gaa tac aat aag aga agg gaa cgg gaa cta aga cgg aaa cat   2232
210 Gln Leu Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu Arg Arg Lys His
211     690             695             700
213 gtc atg gaa gtt cga cag cag cct aag agt ttg aag tct aaa gaa ctc   2280
214 Val Met Glu Val Arg Gln Gln Pro Lys Ser Leu Lys Ser Lys Glu Leu
215 705             710             715             720
217 caa ata aaa aag cag ttt cag gat acc tgc aaa att caa acc aga cag   2328
218 Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Ile Gln Thr Arg Gln
219             725             730             735
221 tac aaa gca tta agg aat cac cta ctg gag act aca cca aag agt gag   2376
222 Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys Ser Glu
223             740             745             750
225 cac aaa gct gtt ctg aaa aga ctc aag gag gaa cag act cgg aag tta   2424
226 His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg Lys Leu
227         755             760             765
229 gcc atc ttg gct gag cag tat gat cat agc att aat gaa atg ctc tcc   2472
230 Ala Ile Leu Ala Glu Gln Tyr Asp His Ser Ile Asn Glu Met Leu Ser
231     770             775             780
233 aca caa gct ctg cgt ttg gat gaa gca cag gaa gca gaa tgc cag gtt   2520
234 Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Val
235 785             790             795             800
237 ttg aag atg cag cta cag cag gaa ctg gag ctg ttg aat gca tat cag   2568
238 Leu Lys Met Gln Leu Gln Gln Glu Leu Glu Leu Leu Asn Ala Tyr Gln
239             805             810             815
241 agc aaa atc aag atg cag gct gag gcc caa cat gat cga gag ctt cga   2616
242 Ser Lys Ile Lys Met Gln Ala Glu Ala Gln His Asp Arg Glu Leu Arg
243             820             825             830
245 gag ctg gaa caa agg gtc tcc ctt cgg aga gca ctc tta gaa cag aag   2664
246 Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu Leu Glu Gln Lys
247         835             840             845
249 att gaa gaa gag atg ttg gct ttg cag aat gaa cgc aca gaa cga ata   2712
250 Ile Glu Glu Glu Met Leu Ala Leu Gln Asn Glu Arg Thr Glu Arg Ile
251     850             855             860
253 cgt agc ctg ctc gag cgc cag gcc aga gaa att gaa gct ttt gac tct   2760
254 Arg Ser Leu Leu Glu Arg Gln Ala Arg Glu Ile Glu Ala Phe Asp Ser
255 865             870             875             880
257 gaa agc atg aga tta ggt ttt agt aac atg gtc ctt tct aat ctc tcc   2808
258 Glu Ser Met Arg Leu Gly Phe Ser Asn Met Val Leu Ser Asn Leu Ser
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259                 885              890              895
261 cct gag gca ttc agc cac agc tac cca gga gct tct agc tgg tct cac  2856
262 Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His
263             900              905              910
265 aat cct act ggg ggt tca gga cct cac tgg ggt cat ccc atg ggt ggc  2904
266 Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly
267         915              920              925
269 aca cca caa gct tgg ggt cat ccg atg caa ggc gga ccc caa cca tgg  2952
270 Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp
271     930              935              940
273 ggt cac ccc tca ggg cca atg caa ggg gta cct cga ggt agc agt ata  3000
274 Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile
275 945              950              955              960
277 gga gtc cgc aat agc ccc cag gct ctg agg cgg aca gct tct ggg gga  3048
278 Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly
279             965              970              975
281 cgg acg gaa cag ggc atg agc aga agc acg agt gtc act tca caa ata  3096
282 Arg Thr Glu Gln Gly Met Ser Arg Ser Thr Ser Val Thr Ser Gln Ile
283         980              985              990
285 tcc aat ggg tca cac atg tct tac aca taataattga aagtggcaat        3143
286 Ser Asn Gly Ser His Met Ser Tyr Thr
287         995             1000
289 tccgctggag ctgtctgcca aaagaaactg cctacagaca tcagcacagc agcctcctca 3203
291 cttgggtact accgggtgga agctgtgcat atggtatatt ttattcgtct ttgtaaagcg 3263
293 ttatgttttg tgtttactaa ttgggatgtc atagtatttg gctgccggg            3312
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296 <210> SEQ ID NO: 2
297 <211> LENGTH: 1001
298 <212> TYPE: PRT
299 <213> ORGANISM: Rattus norvegicus
301 <400> SEQUENCE: 2

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302 Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala
303   1               5              10              15
305 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg
306             20              25              30
308 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
309         35              40              45
311 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
312     50              55              60
314 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
315 65              70              75              80
317 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
318             85              90              95
320 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
321             100              105              110
323 Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
324     115              120              125
326 Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
327     130              135              140
329 His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/08/2004
PATENT APPLICATION: **US/09/686,346B**   TIME: 16:10:20

Input Set : **D:\Utsd1276.app**
Output Set: **N:\CRF4\04082004\I686346B.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 5,92,138
Seq#:7; N Pos. 208,210,223
Seq#:10; N Pos. 192
Seq#:11; N Pos. 18
Seq#:19; N Pos. 24,31
Seq#:20; N Pos. 3,6,13,16,19
Seq#:21; N Pos. 11,14,18
Seq#:22; N Pos. 19,22

VERIFICATION SUMMARY   DATE: 04/08/2004
PATENT APPLICATION: **US/09/686,346B**   TIME: 16:10:20

Input Set : **D:\Utsd1276.app**
Output Set: **N:\CRF4\04082004\I686346B.raw**

L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:180
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0